Atlas of Genetics and Cytogenetics in Oncology and Haematology

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Gene Section

Mini Review

ORAOV1 (oral cancer overexpressed 1)

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Identity

Other names: TAOS1

HGNC (Hugo): ORAOV1

Location: 11q13.2

DNA/RNA

Note

The ORAOV1 gene spans 9.75 Kb genomic DNA and consists of 5 known exons. The coding sequence of ORAOV1 is 414 nucleotides long.

Transcription

So far, there is one reported transcript variant of ORAOV1 caused by alternative exon utilization. The production of transcript variant 1, which is

named as ORAOV1-A, is produced by alternative splicing of exon 3. An in-frame stop codon in exon 4 indicates that the ORAOV1 protein isoform 1 may be interrupted at this position. Interestingly, an association between the expression level of this ORAOV1 gene ORAOV1-A and the differentiation degree of oral squamous cell carcinoma has been observed in a Chinese patient cohort.

Protein

Note

So far, no study describes the location of ORAOV1 protein in cells or tissues.

Function

Apoptosis, but whether it belongs to extrinsic or intrisic pathway is yet unknown.

Implicated in

Oral squamous cell carcinoma

Note

ORAOV1 gene may be a candidate biomarker for diagnosis and prognosis in oral squamous cell carcinoma (OSCC). This finding was made based on a study using PCR to measure ORAOV1 in 15 healthy oral mucosa tissue samples, 30 OLK tissues samples, and 33 OSCC tissue samples.

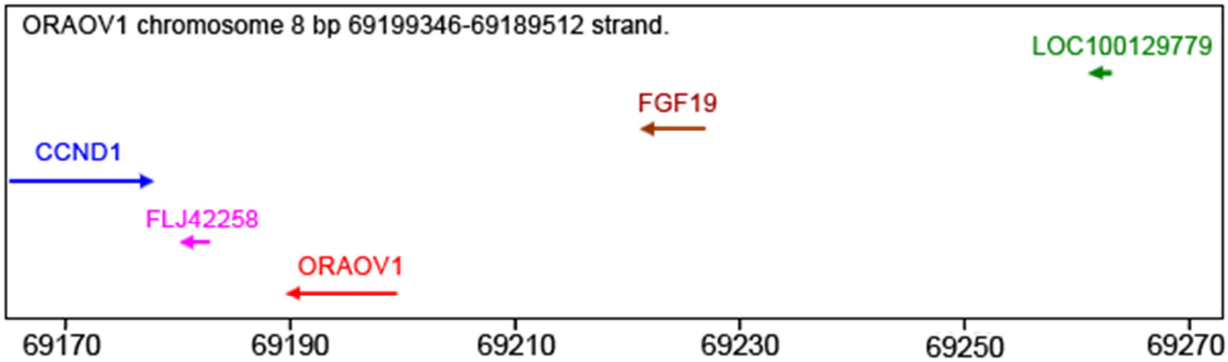


Fig. 1

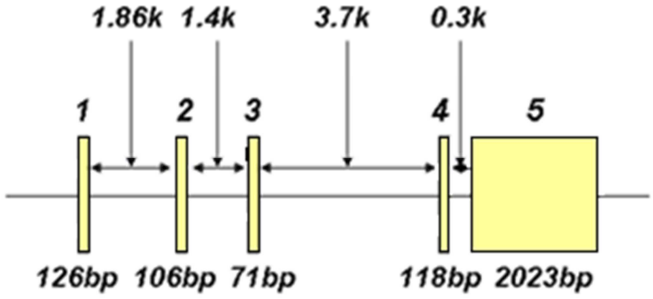
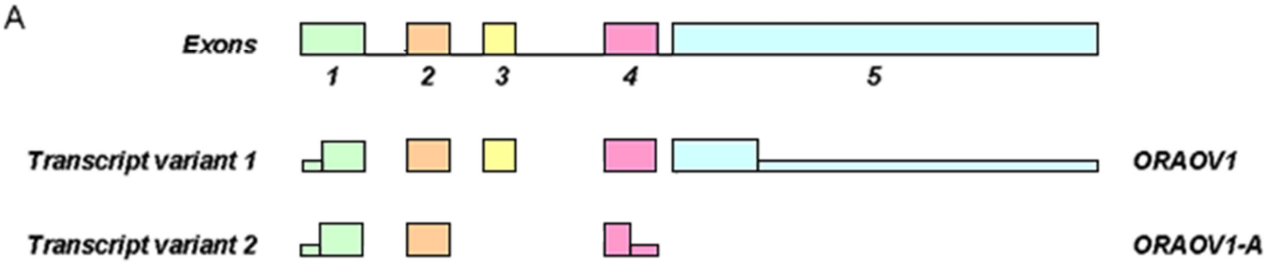


Fig. 2



B

ORAOV1 1 MAGSQDIFDAIVMADERFHGEGYREGYEEGSSLGVMEGRQHGTLHGAKIGSE IGCYQGFA 60
ORAOV1-A 1 MAGSQDIFDAIVMADERFHGEGYREGYEEGSSLGVMEGRQHGTLHGAKIGSE QKDEGLRI 60

ORAOV1 61 FAWKCLLHSCTTEKDSRKMKVLESLIGMIQKFPYDDPTYDKLHEDLDKIRGKFKQFCSLL 120
ORAOV1-A 61 IDWNDPEIPL 70

ORAOV1 121 NVQPDFKISAEGSGLSF 137

Figure 1 : ORAOV1 gene consists of five exons and spans 9.75 kb of genomic DNA.
Figure 2 : (A) The schematic structures of the ORAOV1 gene and its two transcript variants. ORAOV1 has five exons. The two ORAOV1 splice variants consist of different exon combinations that produce different protein-coding regions. (B) Comparison of ORAOV1 with ORAOV1-A nucleotide sequence. White boxes show amino acid differences.

The authors found that ORAOV1 amplification was significant-ly associated with larger tumor size, presence of lymph node metastasis, poor histological differen-tiation and advanced clinical stage. Therefore, they suggested the potential roles of ORAOV1 in oral carcinogenesis. Further studies about the biological functional role of ORAOV1 in OSCC tumori-genesis showed that ORAOV1 plays pivotal roles in the growth and angiogenesis of OSCC. The authors performed a loss-of-function study by using small interfering RNA (siRNA) against ORAOV1 in two OSCC cell lines. They found that the OSCC cells with reduced ORAOV1 showed retarded cell growth in vitro and displayed inhibition in both tumor growth and tumor angiogenesis in vivo. Further analyses reveal that the retarded cell growth is associated with an increase in apoptosis involving the activation of caspase 3-dependent pathway, and a cell cycle arrest at the S-phase with a downregulation of cyclin A, cyclin B1, and CDC2. The suppressed tumor growth in vivo may be attributed to synergistic effect between inhibition in cell growth and suppression of tumor angio-genesis. The latter is most likely due to a suppression of VEGF.

The study of the novel splice variant of ORAOV1, ORAOV1-A, showed that there was an inverse correlation between the expression frequency of ORAOV1-A and the degree of differentiation in OSCC. This result suggested that ORAOV1-A may play a functional role in the tumorigenesis of OSCC, and the ORAOV1-A expression may serve as an adjunctive prognostic indicator for patients with OSCC.

Esophageal squamous cell carcinoma

Note

ORAOV1 is supposed to serve as a new marker for predicting the malignancy of esophageal SCC. This finding was made based on a study using quantitative RT-PCR to examine the ORAOV1 gene expression level in 38 esophageal SCCs. The authors found that the ORAOV1 overexpression correlated with the clinicopathological features of esophageal SCCs, which revealed a significant difference in lymph node metastasis and a trend towards advanced TNM stages.

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